

162174

From: Bowman, Amy
Sent: Wednesday, September 28, 2005 3:01 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/738,413

Hello,
I need SEQ ID NO: 1 searched in application 10/738,413, with lower and upper limits of 21 and 30 nucleobases, respectively.

Thank you,
Amy Bowman
AU 1635
REM 2C31
mail REM 2C18
571-272-0755

CRFE

Barb O Breyer

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: September 30, 2005, 09:06:54 ; Search time 1712 Seconds
(without alignments)
594.369 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uaggaccugccagucutt 21

Scoring table: IDENTITY_NUC

Gapext 1.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 646394

Minimum DB seq length: 21

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pv:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_uu:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	13.6	64.8	25 AR091153	AR091153 Sequence
C 2	13.6	64.8	26 AR091206	AR091206 Sequence
C 3	13.6	64.8	26 AR198188	AR198188 Sequence
C 4	13.6	64.8	25 AR198241	AR198241 Sequence
C 5	13.6	64.8	26 AR260342	AR260342 Sequence
C 6	13.6	64.8	26 AR260395	AR260395 Sequence
C 7	13.4	63.8	23 AR526958	AR526958 Sequence
C 8	13.4	63.8	25 128239	128239 Sequence
C 9	13.4	63.8	25 AR195002	AR195002 Sequence
C 10	13.4	63.8	29 AX183809	AX183809 Sequence
C 11	13.2	62.9	22 E26686	E26686 Improved
C 12	13.2	62.9	24 AX292533	AX292533 Sequence
C 13	12.8	61.0	21 BD171375	BD171375 Method fo
C 14	12.8	61.0	21 BD173609	BD173609 Method of
C 15	12.8	61.0	22 AX334409	AX334409 Sequence
C 16	12.8	61.0	25 CQ86237	CQ86237 Sequence
C 17	12.6	60.0	22 AX503893	AX503893 Sequence
C 18	12.6	60.0	23 AX148231	AX148231 Sequence
C 19	12.6	60.0	23 AX473373	AX473373 Sequence

ALIGNMENTS									
RESULT 1									
AR091153/c	AR091153	LOCUS	Sequence	1273	from patent	26 bp	DNA	linear	PAT 07-SEP-2000
		DEFINITION							
		ACCESSION	AR091153						
		VERSION	AR091153..1	GI:10017908					
		KEYWORDS							
		SOURCE	Unknown.						
		ORGANISM	Unclassified.						
		REFERENCE	1 (bases 1 to 26)						
		AUTHORS	Chenchik,A., Jokhadze,G. and Bibilashvili,R.						
		TITLE	Methods of assaying differential expression						
		JOURNAL	Patent: US 5994076A 1273 30-NOV-1999;						
		FEATURES							
		SOURCE	1. .26 /organism="unassigned DNA"						
		ORIGIN							
		Query	Match	64.8%	Score	13.6;	DB 6;	Length 26;	
		Best	Local Similarity	55.0%	Pred. No.	1.5e+04	;	Indels 0;	Gaps 0;
		Matches	11; Conservative	5;	Mismatches	4;			
	QY	1	UAGGACCUCCAGUCUTT	20					
		:	: : :						
	Db	20	TTCGGCTTGCCGGTGCTTT	1					
		RESULT 2							
		AR091206	AR091206	LOCUS	Sequence	1326	from patent	26 bp	DNA
									linear
									PAT 07-SEP-2000
		DEFINITION	AR091206	SEQUENCE	ACCESSION	AR091206..1	GI:10017961		
		KEYWORDS							
		SOURCE	Unknown.						
		ORGANISM	Unclassified.						
		REFERENCE	1 (bases 1 to 26)						
		AUTHORS	Chenchik,A., Jokhadze,G. and Bibilashvili,R.						
		TITLE	Methods of assaying differential expression						

	JOURNAL FEATURES source	Patent: US 5994076-A 1326 30-NOV-1999; Location/Qualifiers 1..26 /organism="unknown" /mol_type="unassigned DNA"	RESULT 5 AR260342/c LOCUS AR260342 Sequence 1273 from patent US 6489455. DEFINITION AR260342 ACCESSION AR260342 VERSION AR260342.1 GI:27310853 KEYWORDS SOURCE Unknown. ORGANISM Unknown.	linear	PAT 20-DEC-2002
ORIGIN					
Qy	2	Query Match Best Local Similarity 64.8%; Score 13.6; DB 6; Length 26; Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	Result 3 AR198188/c LOCUS AR198188 Sequence 1273 from patent US 6352829. DEFINITION AR198188 ACCESSION AR198188.1 GI:20248037 VERSION AR198188.1 KEYWORDS Unknown. JOURNAL FEATURES source ORGANISM Unclassified. REFERENCE 1 (bases 1 to 26) AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R. TITLE Methods of assaying differential expression JOURNAL Patent: US 632829-A 1273 05-MAR-2002; FEATURES Location/Qualifiers 1..26 /organism="unknown" /mol_type="unassigned DNA"	linear	PAT 20-APR-2002
Db	4	Result 3 AR198188/c LOCUS AR198188 Sequence 1273 from patent US 6352829. DEFINITION AR198188 ACCESSION AR198188.1 GI:20248037 VERSION AR198188.1 KEYWORDS Unknown. JOURNAL FEATURES source ORGANISM Unclassified. REFERENCE 1 (bases 1 to 26) AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R. TITLE Methods of assaying differential expression JOURNAL Patent: US 6489455-A 1273 03-DEC-2002; FEATURES Location/Qualifiers 1..26 /organism="unknown" /mol_type="genomic DNA"	linear	PAT 20-APR-2002	
ORIGIN					
Qy	1	Query Match Best Local Similarity 64.8%; Score 13.6; DB 6; Length 26; Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;	Result 6 AR260395 LOCUS AR260395 Sequence 1326 from patent US 6489455. DEFINITION AR260395 ACCESSION AR260395 VERSION AR260395.1 GI:27310906 KEYWORDS Unknown. JOURNAL FEATURES source ORGANISM Unclassified. REFERENCE 1 (bases 1 to 26) AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R. TITLE Methods of assaying differential expression JOURNAL Patent: US 6489455-A 1326 03-DEC-2002; FEATURES Location/Qualifiers 1..26 /organism="unknown" /mol_type="genomic DNA"	linear	PAT 20-DEC-2002
Db	20	Result 6 AR260395 LOCUS AR260395 Sequence 1326 from patent US 6489455. DEFINITION AR260395 ACCESSION AR260395 VERSION AR260395.1 GI:27310906 KEYWORDS Unknown. JOURNAL FEATURES source ORGANISM Unclassified. REFERENCE 1 (bases 1 to 26) AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R. TITLE Methods of assaying differential expression JOURNAL Patent: US 6489455-A 1326 03-DEC-2002; FEATURES Location/Qualifiers 1..26 /organism="unknown" /mol_type="genomic DNA"	linear	PAT 20-DEC-2002	
RESULT 4					
AR198241	AR198241	Query Match Best Local Similarity 64.8%; Score 13.6; DB 6; Length 26; Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;	Result 4 AR198241 LOCUS AR198241 Sequence 1326 from patent US 6352829. DEFINITION AR198241 ACCESSION AR198241.1 GI:20248090 VERSION AR198241.1 KEYWORDS Unknown. JOURNAL FEATURES source ORGANISM Unclassified. REFERENCE 1 (bases 1 to 26) AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R. TITLE Methods of assaying differential expression JOURNAL Patent: US 632829-A 1226 05-MAR-2002; FEATURES Location/Qualifiers 1..26 /organism="unknown" /mol_type="unassigned DNA"	linear	PAT 20-APR-2002
ORIGIN					
Qy	1	Query Match Best Local Similarity 64.8%; Score 13.6; DB 6; Length 26; Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	Result 7 AR526958/c LOCUS AR526958 Sequence 12 from patent US 6723534. DEFINITION AR526958 ACCESSION AR526958 VERSION AR526958.1 GI:53913871 KEYWORDS Unknown. JOURNAL FEATURES source ORGANISM Unclassified. REFERENCE 1 (bases 1 to 23) AUTHORS Lin,H. TITLE Purified and isolated PIWI family genes and gene products and therapeutic and screening methods using same	linear	PAT 08-OCT-2004
Db	4	Result 7 AR526958/c LOCUS AR526958 Sequence 12 from patent US 6723534. DEFINITION AR526958 ACCESSION AR526958 VERSION AR526958.1 GI:53913871 KEYWORDS Unknown. JOURNAL FEATURES source ORGANISM Unclassified. REFERENCE 1 (bases 1 to 23) AUTHORS Lin,H. TITLE Purified and isolated PIWI family genes and gene products and therapeutic and screening methods using same	linear	PAT 08-OCT-2004	

	JOURNAL FEATURES SOURCE	Patent: US 6723334-A 12-APR-2004; /organism="unknown" /mol_type="Genomic DNA"	RESULT 10 AX183809 AX183809 Sequence 1562 from Patent WO0142511. DEFINITION AX183809 VERSION AX183809.1 GI:1515137 REFERENCE 1. Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K. AUTHORS Ibd-related polymorphisms TITLE PATENT: WO 0142511-A 1562 14-JUN-2001; JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis Biotherapeutics Corporation (CA)	PAT 06-AUG-2001
Qy	2 AGGACCTGGAGTC 16 16 AGGACCTGGAGTC 2	RESULT 8 128239 LOCUS 128239 DEFINITION Sequence 15 from patent US 5569753. ACCESSION 128239.1 VERSION GI:1819015 KEYWORDS JOURNAL SOURCE ORGANISM Unknown. REFERENCE 1. ('bases 1 to 25) AUTHORS Wigler, M. and Lisitsyn, N. TITLE Cancer detection probeB PATENT: US 5569753-A 15 29-OCT-1996; FEATURES location/Qualifiers 1. .25 /organism="unknown" /mol_type="unassigned DNA"	linear PAT 06-FEB-1997	
Qy	1 UAGGACCUCCAGUC 15 1 : : : 3 TAGGAACCTGCCAGTG 17	ORIGIN Query Match Best Local Similarity 63.8%; Score 13.4; DB 6; Length 23; Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0; FEATURES SOURCE ORGANISM Unclassified.	RESULT 11 EZ2686/C LOCUS EZ2686 DEFINITION Improved method for measuring cytokine gene expression. ACCESSION EZ2686 VERSION EZ2686.1 GI:13026773 KEYWORDS JOURNAL JP 1999155600-A/36. SOURCE ORGANISM unidentified REFERENCE 1. ('bases 1 to 22) AUTHORS Michio, S., Takeshi, H., Masato, H. and Hideyuki, I. TITLE Improved method for measuring cytokine gene expression PATENT: JP 1999155600-A 36 15-JUN-1999; JOURNAL SHISEIDO CO LTD COMMENT OS Unidentified PN JP 1999155600-A/36 PD 15-TUN-1999 PP 28-NOV-1997 JP 1997328171 PR PI MICHIRO SHIBATA, TAKESHI HARIYA, MASATO HATAO, HIDEYUKI ICHIKAWA PC C12Q1/68.C07K14/52, C07K14/54, C07K14/55, C07K14/56, C07K14/57, PC C12N15/09, PC G01N33/50 // (C12Q1/68, C12R1:91) CC Strandedness: Single; CC Topology: Linear; PH Key FT Source FT FEATURES SOURCE ORGANISM REFERENCE 1. ('bases 1 to 25) AUTHORS Wigler, M. and Lisitsyn, N. TITLE Cancer detection probeB PATENT: US 6350576-A 24 26-FEB-2002; FEATURES location/Qualifiers 1. .25 /organism="unknown" /mol_type="unassigned DNA"	linear PAT 18-JUN-2001
Qy	1 UAGGACCUCCAGUC 15 1 : : : 3 TAGGAACCTGCCAGTG 17	ORIGIN Query Match Best Local Similarity 73.3%; Score 13.4; DB 6; Length 25; Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	RESULT 10 AX183809 AX183809 Sequence 1562 from Patent WO0142511. DEFINITION AX183809 VERSION AX183809.1 GI:1515137 REFERENCE 1. Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K. AUTHORS Ibd-related polymorphisms TITLE PATENT: WO 0142511-A 1562 14-JUN-2001; JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis Biotherapeutics Corporation (CA)	PAT 06-AUG-2001

Fri Sep 30 14:33:41 2005

us-10-738-413-1.sz21-30.rge

Page 5

Best Local Similarity 62.5%; Pred. No. 4.2e+04;
Matches 10; Conservative 4; Mismatches 2;
Indels 0; Gaps 0;
QY 6 CCUGCCAGUCUCU^T 21
||: |||: |:|||:
Db 19 ACTCCAGAGGCTTT 4

Search completed: September 30, 2005, 11:34:58
Job time : 1716 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6				
Om nucleic - nucleic search, using sw model					
Run on:	September 30, 2005, 09:06:54 ; Search time 415 Seconds (without alignments) 299.553 Million cell updates/sec				
Title:	US-10-738-413-1				
Perfect score:	21				
Sequence:	1 uaggaccugccagucutt 21				
Scoring table:	IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0					
Searched:	4390206 seqs, 2959870667 residues				
Total number of hits satisfying chosen parameters:	1315584				
Minimum DB seq length:	21				
Maximum DB seq length:	30				
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries				
Database :	N_Geneseq_16Dec04:*				
1:	geneseqn1990b:*				
2:	geneseqn1990b:*				
3:	geneseqn2000b:*				
4:	geneseqn2001as:*				
5:	geneseqn2001bs:*				
6:	geneseqn2002as:*				
7:	geneseqn2002bs:*				
8:	geneseqn2003as:*				
9:	geneseqn2003bs:*				
10:	geneseqn2003cb:*				
11:	geneseqn2003cb:*				
12:	geneseqn2004ab:*				
13:	geneseqn2004bs:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	ALIGNMENTS
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
1	14.6	69.5	28	AAH74915	RESULT 1
C	2	14.2	67.6	25 9 ACT63698	AAH74915
C	3	14.2	67.6	28 10 ADK5155	ID AAH74915 standard; DNA; 28 BP.
C	4	14.2	67.6	30 12 ADK45901	XX
C	5	13.8	65.7	22 12 ADK94415	AC AAH74915;
C	6	13.8	65.7	23 5 ADD02074	XX
C	7	13.8	65.7	25 9 ACK1937	DT 29-OCT-2001 (first entry)
C	8	13.8	65.7	25 9 ACT58170	XX
C	9	13.8	65.7	29 10 ADD47044	DE DNA sequence of encoded adaptor for detecting base 1 of template.
C	10	13.8	65.7	29 10 ADK1677	XX
C	11	13.6	64.8	26 6 ABK67185	KW Nucleotide sequence signature; nucleotide sequencing; ss.
C	12	13.6	64.8	26 6 ABK67238	XX OS Synthetic.
C	13	13.6	64.8	28 10 ADD51147	XX
C	14	13.4	63.8	25 2 ART2267	PN WO200161044-A1.
C	15	13.4	63.8	25 2 ART1677	XX
C	16	13.4	63.8	29 4 AAK91238	PR 01-SEP-2000; 2000US-0182454P.
C	17	13.2	62.9	22 2 AAX78420	PA (LYNX-) LYNX THERAPEUTICS INC.
C	18	13.2	62.9	22 2 AAX7938	PI Corcoran KC, Eletr S;
C	19	13.2	62.9	24 6 ABI190987	XX DR WPI: 2001-522608/57.
C	20	13.2	62.9	24 6 ABI190986	PT Determining nucleotide sequence signature, by obtaining optical values for each nucleotide position in a group, adjusting them to get ratio of final highest values near predetermined factor, generating base call.
C	21	13.2	62.9	30 8 AAC80639	PS Disclosure; Page 15; 73pp; English.
C	22	13.2	62.9	21 6 AAI44199	CC The specification describes a method for determining a nucleotide sequence signature. The method comprises obtaining optical measurements with values indicating each nucleotide in a group of nucleotides.
C	23	12.8	61.0	22 6 AAL41637	CC positions, adjusting the values until the ratio of highest value in the set to next highest values in the set is at least a predetermined factor, and generating a base call for a position in the group based on results after the adjustment of values. The method is used for determining a signature of a nucleotide sequence, and for determining a nucleotide
C	24	12.8	61.0	25 9 ACT01231	CC
C	25	12.8	61.0	25 10 ADG14352	CC
C	26	12.8	61.0	25 13 ADC51559	CC
C	27	12.8	61.0	25 13 ADR57519	CC
C	28	12.8	61.0	26 10 ADE40051	CC
C	29	12.8	61.0	26 10 ADE40057	CC
C	30	12.8	61.0	26 10 ADE40055	CC
C	31	12.8	61.0	21 9 AAD58127	CC
C	32	12.6	60.0	21 10 ADD44337	CC
C	33	12.6	60.0	22 6 ABS63481	CC
C	34	12.6	60.0	23 5 ABS07985	CC
C	35	12.6	60.0	23 6 ABQ94689	CC
C	36	12.6	60.0	23 11 ADL96518	CC
C	37	12.6	60.0	23 12 ADQ37704	CC
C	38	12.6	60.0	25 9 ACC42118	CC
C	39	12.6	60.0	25 9 ACI13346	CC
C	40	12.6	60.0	25 9 ACI199905	CC
C	41	12.6	60.0	25 9 ACI63080	CC
C	42	12.6	60.0	25 9 ACI01867	CC
C	43	12.6	60.0	25 9 ACI163699	CC
C	44	12.6	60.0	25 9 ACI163699	CC
C	45	12.6	60.0	30 6 ABK67172	CC

CC sequence of a polynucleotide from a series of optical measurements.
 CC NH74912-27 represent encoded adaptors, which are used for detecting
 CC bases of a DNA template, in the context of the invention
 XX SQ Sequence 28 BP; 4 A; 7 C; 7 G; 7 T; 0 U; 3 Other;
 Query Match 69.5%; Score 14.6; DB 4; Length 28;
 Best Local Similarity 61.9%; Pred. No. 2.8e+03;
 Matches 13; Conservative 4; Mismatches 4;
 Oy 1 UAGGACCUCCAGUGUCUTT 21
 Db 4 :|||:|||:|||:|||:
 Db 4 TAGGAGCTGCCAGTCGCTT 24

RESULT 2
 ACI63698/C
 ID ACI63698 standard; DNA; 25 BP.
 XX
 AC ACI63698;
 XX DT 13-OCT-2003 (first entry)
 DE Human microarray DNA oligonucleotide SEQ ID NO 63689.
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX PR 15-MAR-2002; 2002US-00098263.
 XX PR 16-MAR-2001; 2001US-0276759P.
 XX PA (AFFY-) AFFYMETRIX INC.
 PI Mittmann MP;
 XX DR WPI; 2003-567953/53.
 XX PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT sequence or specific mutations of any gene.
 XX PS Claim 1; SEQ ID NO 63689; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, or to a cDNA library, or to a genomic library. The array is used in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acid probes further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly

CC from USPTO at seqdata.uspto.gov/sequence.html
 XX SQ Sequence 25 BP; 8 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 67.6%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 63.2%; Pred. No. 4.3e+03;
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 GGACCUCCAGUGUCUTT 21
 Db 24 GGACTGACAGIGTCCTT 6

RESULT 3
 ADD5155
 ID ADD5155 standard; DNA; 28 BP.
 XX AC ADD5155;
 XX DE Adapter DNA #10 used to illustrate the method of the invention.
 KW Genetic analysis; allelic analysis; ss.
 XX OS Unidentified.
 FT FH misc_feature Location/Qualifiers
 FT FT /note= "Represented as X2 in the specification"
 PN XX
 PN WO200279496-A2.
 XX PD 10-OCT-2002.
 XX PR 27-MAR-2002; 2002WO-US009928.
 XX PR 28-MAR-2001; 2001US-00821694.
 XX PA (MIND-) APPLIED MINDS INC.
 XX PI Hillis WD;
 XX DR WPI; 2003-046825/04.
 XX PT Obtaining information on target nucleic acid analyte, by hybridizing target with oligonucleotide probes complementary, or complementary except at position of interest to target and analyzing probe hybridization.
 XX PS Example 1; Page 39; 66pp; English.

The invention relates to a method of obtaining information on a target nucleic acid analyte containing a target segment. The method involves hybridising target nucleic acid analyte with at least two oligonucleotide probes, where each probe comprises a sequence fully complementary, or complementary except at a position of interest or variable position, to the target nucleic acid analyte and analysing whether all, some or none of the probes hybridise. The method is useful for sequencing and for obtaining information on a number of target nucleic acid sequence segments, where information comprises the determination of a nucleotide at a position of interest. It is also useful for generic or allelic analysis of genomic DNA or cDNA. The present sequence is an adapter DNA, used to illustrate the method of the invention.

SQ Sequence 28 BP; 4 A; 7 C; 7 G; 6 T; 0 U; 4 Other;
 CC Query Match 67.6%; Score 14.2; DB 10; Length 28;
 CC Best Local Similarity 61.9%; Pred. No. 4.4e+03;
 CC Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 UAGGACCUCCAGUGUCUTT 21
 :|||:|||:|||:|||:

Db 4 KACGGAGCTGCCAGTCCGCTT 24
RESULT 4
 ADP45901
 ID ADP45901 standard; DNA; 30 BP.
 XX
 AC ADP45901;
 DT XX
 26-AUG-2004 (first entry)
 DR PCR Primer 4 used to genotype human MAP kinase MAPK10 polymorphism.
 XX breast cancer; cytostatic; gene therapy; human; ss; primer; PCR; SNP;
 KW single nucleotide polymorphism; MAP kinase; MAPK10; JNK3; JNK3A; p493F12;
 KW p54BSAPK MAP kinase; c-Jun kinase 3; JNK3 alpha protein kinase;
 KW c-Jun N-terminal kinase 3; stress activated protein kinase beta;
 KW chromosome 4q22.1-q23.
 XX Homo sapiens.
 OS
 XX WO2004047623-A2.
 PN XX 10-JUN-2004.
 PD XX 25-NOV-2003; 2003WO-US037948.
 PF XX 25-NOV-2002; 2002US-042913P.
 PR XX 24-JUL-2003; 2003US-0490234P.
 PR XX PA (SEQU-) SEQUENOM INC.
 PA XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R,
 PI XX DR WPI; 2004-441051/41.
 PT XX Identifying a subject at risk of breast cancer by detecting the presence
 PT of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUMA1 or GALE
 PT regions which are associated with breast cancer in a nucleic acid sample
 PT from a subject.
 XX PS Example 5; Page 90; 28pp; English.

XX The invention relates to a novel method for identifying a subject at risk
 CC of breast cancer comprising detecting the presence or absence of one or
 CC more polymorphic variations associated with breast cancer in a nucleic
 CC acid sample from a subject. The method of the invention has cytostatic
 CC applications and may be useful for identifying a subject at risk of
 CC breast cancer, for early diagnosis, prevention and treatment of breast
 CC cancer, possibly via gene therapy, as well as to analyse and predict a
 CC response to a breast cancer treatment, and in clinical drug trials. The
 CC current sequence is that of a PCR primer of the invention which was used
 CC to genotype human MAP kinase MAPK10 (JNK3; JNK3A; p493F12; p54BSAPK MAP
 kinase; 3-JNK3 alpha protein kinase; c-Jun N-terminal kinase 3
 CC ; stress activated protein kinase beta) gDNA which has been mapped to
 CC chromosomal position 4q22.1-q23.
 XX SQ Sequence 30 BP; 7 A; 6 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 12; Length 22;
 Best Local Similarity 64.7%; Pred. No. 6 7e+03;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Oy DE 1 UGGACATGGCCAGAGGU 17
 Db DE 4 TAGGATCTTCAGCTGT 20

RESULT 5
 ADK94415
 ID ADK94415 standard; DNA; 22 BP.
 XX
 AC ADK94415;

Query Match 67.6%; Score 14.2; DB 12; Length 30;
 Best Local Similarity 57.9%; Pred. No. 4.4e+03;
 Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Oy DE 1 UGGACCCAGCAGUCU 19
 Db DE 4 TTGGATGTCGCCAGGCTT 22

XX WO20066737-A1.
 PN XX 09-NOV-2000.
 PD XX 05-APR-2000; 2000WO-US009178.
 PF XX

XX 06-MAY-2004 (first entry)
 DT XX
 DE XX Primer of the invention #135.
 XX KW human; single nucleotide polymorphism; SNP; ss; primer.
 KW XX OS Synthetic.
 KW XX JP2003259875-A.
 PN XX DR 16-SEP-2003.
 PD XX PS 08-MAR-2002; 2002JP-00064373.
 PF XX 08-MAR-2002; 2002JP-00064373.
 PR XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA XX DR WPI; 2004-093977/10.
 PT XX Novel polynucleotide useful for PCR amplification along with two DNA
 PT fragment from another set of sequences, or for detecting single
 PT nucleotide polymorphism in human gene.
 XX PS XX Claim 2; SEQ ID NO 3444; 2627pp; Japanese.
 CC The present invention relates to a polynucleotide isolated from a human
 CC gene and is useful for detecting a single nucleotide polymorphism in a
 CC human gene or for diagnosing of disease. The invention enables the
 CC detection of a single nucleotide polymorphism in a human gene. The
 CC present sequence represents a primer of the invention.
 CC XX Sequence 22 BP; 3 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
 CC Query Match 65.7%; Score 13.8; DB 12; Length 22;
 CC Best Local Similarity 64.7%; Pred. No. 6 7e+03;
 CC Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 CC Oy DE 1 UGGACATGGCCAGAGGU 17
 CC Db DE 4 TAGGATCTTCAGCTGT 20

RESULT 6
 ADP02074/c
 ID ADP02074 standard; DNA; 23 BP.
 XX AC ADP02074;
 XX DT 26-MAR-2001 (first entry)
 XX 3' PCR primer for preparing N-myc fusion construct.
 DE XX Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
 KW TNF-Receptor associated factor; TRAF2 truncated; TRAF2TR; TRAF2TD;
 KW TRAF2 truncated-deleted; antiinflammatory; cardiot; Myc tag; vasoactive;
 KW antisporadic; antirheumatic; antiarthritic; antiangiogenic; antiidiabetic;
 KW antiatherosclerotic; immunosuppressive; Crohn's disease; psoriasis;
 KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
 KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
 KW neurodegenerative disease; congestive heart failure; PCR primer;
 KW myocardial infarction; nuclear factor kappa B; NFkB; ss.
 KW XX Homo sapiens.
 OS OS Synthetic.

PR 30-APR-1999; 99US-0131940P.
 XX PR
 PA (AVET) AVENTIS PHARM PROD INC.
 XX PR
 PT searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
 XX PI
 DR WPI; 2001-007223/01.
 XX PR
 PT New nucleic acid encoding variants of tumor necrosis factor receptor associated factors useful for inhibiting tumor necrosis factor alpha-regulated pathways, and for treating Crohn's disease, psoriasis, and rheumatoid arthritis.
 XX PS Example 3; Page 42; 74pp; English.
 XX CC The present invention relates to variants of tumor necrosis factor (TNF) receptor associated factor (TRAF2). TRAF2 has two variants, a splice variant referred as "TRAF2 truncated" (TRAF2TR) and an expression construct with enhanced dominant negative properties referred as "TRAF2 truncated-deleted" (TRAF2DT). TRAF2 variants are capable of inhibiting TNF alpha signalling pathway and for inhibiting diseases involving over production of TNFalpha, TNFalpha pathologies involving hyperactivation of nuclear factor kappa B (NFkB). The variants are also useful for inhibiting and treating inflammatory processes involving TNFalpha such as Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host disease, non-insulin dependent diabetes, inflammatory bowel disease, and neurodegenerative diseases or cardiovascular disease such as cardiac ischaemia-reperfusion injury following myocardial infarction, coronary artery bypass surgery, cardiac transplantation or ischaemia-reperfusion injury in the central nervous system (CNS) following stroke, the progression and rupture of advanced coronary atherosclerotic plaques, development and progression of congestive heart failure, endothelial cell injury following balloon angioplasty, or apoptotic cell death of myocardial cells. The present sequence is a 3' PCR primer for preparing a fusion construct containing N-myc affinity tag as well as truncated and full length TRAF2. N-myc is useful for determining the effect of TRAF2TR on NFkB activation. Truncated as well as full length TRAF2 were constructed with N-myc affinity tags in a mammalian expression vector (pcDNA3). N-myc fusion constructs were prepared using 5' and 3' PCR primers.

CC SQ Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

CC Query Match Best Local Similarity 65.7%; Score 13.8; DB 5; Length 23; Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 3 SGACCTGGCAAGCCU 19

CC Db 19 GGACCTGACAGGCTC 3

RESULT 7 ACK21937/c ID ACK21937 standard; DNA; 25 BP.
 XX AC ACK21937;
 XX DT 14-OCT-2003 (first entry)
 XX DE Human microarray DNA oligonucleotide SEQ ID NO 121918.
 XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
 XX OS Homo sapiens.
 XX PN US2003104410-A1.
 XX PD 05-JUN-2003.
 XX PP 15-MAR-2002; 2002US-00098263.
 XX PR 15-MAR-2002; 2002US-00098263.

XX PS Claim 1; SEQ ID NO 121918; 9pp; English.
 XX CC The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, Perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic marker or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in *in situ* hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

Query Match Best Local Similarity 65.7%; Score 13.8; DB 9; Length 25; Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 4 GACCUGGCAGUCUCU 20

Db 21 GACCTGGCAAGACTCT 5

RESULT 8 AC158170/c ID AC158170 standard; DNA; 25 BP.
 XX AC AC158170;
 XX DT 13-OCT-2003 (first entry)
 XX DE Human microarray DNA oligonucleotide SEQ ID NO 58161.
 XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression; generic variation; biallelic marker; polymorphism; human; cross-species comparison.
 XX OS Homo sapiens.
 XX PN US2003104410-A1.
 XX PD 05-JUN-2003.
 XX PP 16-MAR-2001; 2001US-0276759P.

XX
PA
(AFFY-) AFFYMATRIX INC.
XX
PT
Mittmann MP;
XX
DR
WPI; 2003-567953/53.

XX
PT
New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
XX
PS
Claim 1; SEQ ID NO 58161; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

XX
SQ Sequence 25 BP; 8 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 70.6%; Pred. No. 6.8e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACCUGGCCAGUGCUCUTT 21
DB 25 ACCAGGCCAGTGTCTT 9

RESULT 9
ADC47044
ID ADC47044 standard; DNA; 29 BP.
XX
AC
ADC47044;
XX
DT 22-APR-2004 (first entry)

XX
ID ADI35763
ID ADI35763 standard; DNA; 29 BP.
XX
AC
ADI35763;
XX
DT 22-APR-2004 (first entry)

XX
DB Human potassium channel protein BEC1 related PCR primer SEQ ID NO:6.
XX
KW transgenic animal; potassium channel; BEC1; nootropic; tranquiliser; dementia; memory loss; anxiety; learning ability; human; PCR; ss; primer.
XX
OS Homo sapiens.
XX
Synthetic.
XX
PN WO2003041496-A1.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-JP011943.
XX
PR 14-NOV-2001; 2001JP-00349288.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PT Miyake A, Nakamura Y, Ni J, Mochizuki S;
XX
DR WPI; 2003-457459/43.

PT Transgenic animal overexpressing potassium channel protein BEC1 for screening potential treatments for dementia and anxiety.

XX
PS Example 1; SEQ ID NO 6; 5pp; Japanese.

CC The present invention describes a transgenic animal transformed by a promoter together with a polynucleotide encoding potassium channel protein BEC1 or encoding a protein derived from BEC1 by addition, deletion and/or substitution of up to ten amino acid residues and at least 90% homologous to it. Also described: (1) screening (M1) for substances for the treatment of dementia, memory loss and anxiety using the transgenic animal as a disease model; and (2) the preparation (M2) of drug compositions containing as active components substances identified by (M1). BEC1 has nootropic and tranquilliser activities. The transgenic

XX
PI Kubota H, Suzuki T, Miura M, Nakai E, Yahiro K, Miyake A;
PT Mochizuki S, Nakatou K;
XX
DR WPI; 2003-697418/66.

XX
PT Antidementia agents comprise new and known brain-specific eag-like channel 1 (BEC1) potassium channel inhibitors.
XX
PS Disclosure; Page 90; 95pp; Japanese.

XX
CC The invention relates to an antidementia agent that comprises a brain-specific eag-like channel 1 (BEC1) potassium channel inhibitor. Agents of the invention are used as BEC1 potassium channel inhibitors for treating and preventing dementia and learning disabilities. The current sequence represents the BEC1 potassium channel inhibitor related PCR primer sequence.

XX
SQ Sequence 29 BP; 3 A; 11 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 10; Length 29;
Best Local Similarity 70.6%; Pred. No. 6.9e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCUGCCAGUSCUCUT 20
DB 8 GACCTGCCCCGTGCTCT 24

RESULT 10
XX
ID ADI35763
ID ADI35763 standard; DNA; 29 BP.
XX
AC
ADI35763;
XX
DT 22-APR-2004 (first entry)

XX
DB Human potassium channel protein BEC1 related PCR primer SEQ ID NO:6.
XX
KW transgenic animal; potassium channel; BEC1; nootropic; tranquiliser; dementia; memory loss; anxiety; learning ability; human; PCR; ss; primer.
XX
OS Homo sapiens.
XX
Synthetic.
XX
PN WO2003041496-A1.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-JP011943.
XX
PR 14-NOV-2001; 2001JP-00349288.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PT Miyake A, Nakamura Y, Ni J, Mochizuki S;
XX
DR WPI; 2003-457459/43.

PT Transgenic animal overexpressing potassium channel protein BEC1 for screening potential treatments for dementia and anxiety.

XX
PS Example 1; SEQ ID NO 6; 5pp; Japanese.

CC The present invention describes a transgenic animal transformed by a promoter together with a polynucleotide encoding potassium channel protein BEC1 or encoding a protein derived from BEC1 by addition, deletion and/or substitution of up to ten amino acid residues and at least 90% homologous to it. Also described: (1) screening (M1) for substances for the treatment of dementia, memory loss and anxiety using the transgenic animal as a disease model; and (2) the preparation (M2) of drug compositions containing as active components substances identified by (M1). BEC1 has nootropic and tranquilliser activities. The transgenic

XX
PT WO2003066099-A1.
XX
DD 14-AUG-2003.
XX
PP 03-FEB-2003; 2003WO-JP001065.
XX
PR 05-FEB-2002; 2002JP-00028844.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.

QY	2 AGGACCCUGGCCAGUCUTT 21	Query Match	64.8%	Score 13.6;	DB 6;	Length 26;
Best Local Similarity	65.0%	Pred. No.	8.5e+03;	Indels	0;	Gaps 0;
Matches	13;	Conservative	3;	Mismatches	3;	
DB	4 AGGACCTTCAGTCCACTT 23					
DS		RESULT 13				
XX		AAD5147				
XX		ID AAD5147 Standard; DNA; 28 BP.				
XX		AAD5147;				
XX		02-APR-2003 (first entry)				
XX		Adapter DNA #2 used to illustrate the method of the invention.				
XX		Genetic analysis; allelic analysis; SB.				
XX		Unidentified.				
DS						
XX		Key	Location/Qualifiers			
XX		modified_base	4			
XX		/tag= a				
XX		/mod_base= OTHER				
XX		/note= "8-oxo-dG"				
XX		WO200279496-A2.				
PN		PP	27-MAR-2002; 2002WO-US009928.			
XX		PR	28-MAR-2001; 2001US-00821694.			
XX		PT	(MIND-) APPLIED MINDS INC.			
XX		PT	Hillis WD;			
XX		DR	WPI; 2003-046825/04.			
XX		PS	Obtaining information on target nucleic acid analyte, by hybridizing target with oligonucleotide probes complementary, or complementary except at position of interest to target and analyzing probe hybridization.			
XX		Example 1; Page 39; 66pp; English.				
CC		The invention relates to a method of obtaining information on a target nucleic acid analyte containing a target segment. The method involves hybridising target nucleic acid analyte with at least two oligonucleotide probes, where each probe comprises a sequence fully complementary, or complementary except at a position of interest or variable position, to the target nucleic acid analyte and analysing whether all, some or none of the probes hybridise. The method is useful for sequencing and for obtaining information on a number of target nucleic acid sequence segments, where information comprises the determination of a nucleotide at a position of interest. It is also useful for genetic or allelic analysis of genomic DNA or cDNA. The present sequence is an adapter DNA, used to illustrate the method of the invention.				
CC		Sequence 28 BP; 4 A; 7 C; 8 G; 6 T; 0 U; 3 Other;				
CC		Query Match 64.8%; Score 13.6; DB 10; Length 28;				
CC		Best Local Similarity 65.0%; Pred. No. 8.6e+03; Indels 0; Gaps 0;				
CC		Matches 13; Conservative 3; Mismatches 3;				
CC		2 AGGACCCUGGCCAGUCUTT 21				
CC		5 ACAGGCTGCGACTCCGCTT 24				

ID	AAT32267	standard; DNA; 25 BP.	XX	RESULT 14		
XX						
AC						
AA	AAT32267;					
XX						
DT	07-JAN-1997	(first entry)				
XX						
DE	Probe for the detection of lesions associated with neoplastic cells.					
XX						
KW	Probe; detection; lesion; neoplasia; neoplastic cells; cancer; prognosis;					
KW	therapy; tumour cell; tumour; homozygous loss; ss.					
XX						
OS	Synthetic.					
XX						
PN	WQ961989-A1.					
XX						
PD	27-JUN-1996.					
XX						
PF	20-DEC-1995;	95WO-US016766.				
XX						
PR	20-DEC-1994;	94US-00360096.				
XX						
PA	(COLD-) COLD SPRING HARBOR LAB.					
XX						
PT	Wigler M, Lisickyn N;					
XX						
DR	WPI; 1996-309603/31.					
XX						
PT	Nucleic acid sequence probes - are used for the detection of lesions					
PT	associated with neoplastic cells.					
XX						
PS	Claim 1; Page 23; 31pp; English.					
XX						
CC	The nucleic acid sequence probes described in AAT32244-78 are used for					
CC	the detection of lesions associated with neoplastic cells. The sequences					
CC	can be used for identifying the locus associated with the lesion, for					
CC	determining cancer susceptibility of cells, as well as categorising and					
CC	characterising tumour cells for prognosis and therapy. Two probes					
CC	(AAT32267, AAT32268) were used to detect homozygous loss in tumour cell					
CC	lines at chromosome location 18					
XX						
SQ	Sequence 25 BP; 5 A; 5 C; 8 G; 7 T; 0 U; 0 Other;					
XX						
QY	Query Match	63.84%	Score 13.4;	DB 2;	Length 25;	
QY	Best Local Similarity	73.34%	Pred. No. 1.1e+04;			
QY	Matches	11;	Conservative	3;	Mismatches	
Db	1 UAGGACCCGGCAUG	15				
Db	: : : :	17				
Db	3 TAGGAACCTGCCAGTG	17				
RESULT 15						
AATT71677						
ID	AATT71677 standard; DNA; 25 BP.					
XX						
AC						
XX						
AA	AATT71677;					
XX						
DT	04-FEB-1998	(first entry)				
XX						
DE	Cancer detection probe VAKO441-9 PCR 5' primer.					
XX						
KW	PCR primer; VAKO441-9; detection; neoplastic; lesion; tumour; RDA;					
KW	homozygous loss; representational difference analysis; probe;					
XX						
OS	Synthetic.					
OS	Homo sapiens.					
XX						
PN	WQ972271-A2.					
XX						
PD	26-JUN-1997.					
XX						

PP 20-DEC-1996; 96WO-US020631.
 XX
 PR 21-DEC-1995; 95US-00576202.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Wigler M, Lisitsyn N;
 XX
 DR WPI; 1997-341709/31.

XX

PT New cancer detection probes - useful for detecting genomic lesions
 PT associated with neoplasia in human cells, e.g. for detection, prognostic
 and therapy of cancer.

XX

PS Claim 10; Page 23; 32pp; English.

XX
 CC This Primer is used to amplify a PCR product of 244 bp used as a probe in
 a standard PCR panel for determination of a lesion associated with
 neoplasia in human cells. In particular, this probe identifies a
 CC homozygous loss in tumour cell line at chromosome location 18. The DNA
 CC can be obtained by standard representative difference analysis (RDA).
 CC RDA was performed using Bgl II restriction endonuclease on tumour DNA
 CC (driver) and matched with normal DNA (tester). Pure tumour DNA of the
 CC RDA difference products were cloned into plasmids. Selected plasmid
 CC inserts were analysed by Southern blot hybridisation. Oligonucleotides
 CC synthesised from selected plasmid insert sequences were used to screen a
 CC standard PCR panel of DNAs from tumour cell lines and a control DNA.
 CC Probes were subsequently mapped to human chromosomes by PCR using an
 CC existing panel of human, rodent somatic cell hybrids. The DNA can be used
 CC for detecting genomic lesions associated with cancer and for prognosis
 CC and therapy. The DNA sequences can also be used to obtain other suitable
 CC probes by walking genomic DNA to obtain a secondary probe, and repeating
 CC the walking to obtain successive probes which are screened with normal
 CC and tumour cells
 XX

SQ Sequence 25 BP; 5 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 63.8%; Score 13.4; DB 2; Length 25;
 Best Local Similarity 73.3%; Pred. No. 1.1e+04;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 UGGACCCUGCCAGUG 15
 Db ;||||| :||||| :|||:
 3 TAGGAACTGCCAGTG 17

Search completed: September 30, 2005, 09:14:08
 Job time : 421 secs

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OM nucleic - nucleic search, using SW model

Run on: September 30, 2005, 09:06:54 ; Search time 123 Seconds
(without alignments)
279.364 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uaggacucugccagucucutt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818133359 residues

Total number of hits satisfying chosen parameters: 569154

Minimum DB seq length: 21
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgtn2_6/ptodata/1/ina/5A_COMB.seq: *
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3: /cgtn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgtn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgtn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgtn2_6/ptodata/1/ina/backtlesl.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	15.8	75.2	25	4	US-09-396-196G-107545		Sequence 107545, Application US/09396196G
2	14.8	70.5	25	4	US-09-396-196G-40269		Sequence 40269, A
3	14.8	70.5	25	4	US-09-396-196G-55195		Sequence 55195, A
4	14.8	70.5	25	4	US-09-396-196G-55196		Sequence 55196, A
5	14.4	68.6	25	4	US-09-396-196G-48277		Sequence 48277, A
6	14.4	68.6	25	4	US-09-396-196G-107546		Sequence 107546, A
7	14	66.7	25	4	US-09-396-196G-48278		Sequence 48278, A
8	14	66.7	25	4	US-09-396-196G-52121		Sequence 52121, A
9	14	66.7	25	4	US-09-396-196G-52122		Sequence 52122, A
10	13.6	64.8	26	2	US-08-859-98-1273		RESULT 2
11	13.6	64.8	26	2	US-08-859-98-1326		US-09-396-40269
12	13.6	64.8	26	3	US-09-225-92-1273		Sequence 40269, Application US/09396196G
13	13.6	64.8	26	3	US-09-225-28-1326		Sequence 1273, AP
14	13.6	64.8	26	4	US-09-225-20-B-1273		Sequence 1273, AP
15	13.6	64.8	26	4	US-09-225-201B-1226		Sequence 1326, AP
16	13.4	63.8	23	4	US-09-873-37A-12		Sequence 1326, AP
17	13.4	63.8	25	1	US-08-360-09-15		Sequence 1273, AP
18	13.4	63.8	25	3	US-08-576-202-24		Sequence 1326, AP
19	13.4	63.8	25	4	US-09-396-196G-48276		Sequence 1326, AP
20	13.4	63.8	25	4	US-09-396-196G-11276		Sequence 1326, AP
21	13.4	63.8	25	4	US-09-396-196G-124290		Sequence 1326, AP
22	13.4	63.8	25	4	US-09-396-196G-124290		Sequence 1326, AP
23	13.2	62.9	25	4	US-09-396-196G-18422		Sequence 18422, A
24	13.2	62.9	25	4	US-09-396-196G-18423		Sequence 18423, A
25	13.2	62.9	25	4	US-09-396-66673		Sequence 66673, A
26	13.2	62.9	25	4	US-09-396-196G-66674		Sequence 66674, A
27	13.2	62.9	25	4	US-09-396-196G-66674		Sequence 66674, A

ALIGNMENTS

RESULT 1
US-09-396-196G-107545
; Sequence 107545, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Methods of Genetic Analysis
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 107545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus

US-09-396-196G-107545
Query Match 75.2%; Score 15.8; DB 4; length 25;
Best Local Similarity 68.4%; Pred. No. 1.9e+22; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 4; Sequence 107545, A

OY 2 AGGAGCTGCCAGCAGUCUT 20
Db 1 AAGAGCTGCCAGTCCTT 19

APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIORITY FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 40269

; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101_1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO: 52122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-48278

US-09-396-196G-52121

; QUERY MATCH:
; Query Match 66.7%; Score 14; DB 4; Length 25;
; Best Local Similarity 71.4%; Pred. No. 1.4e+03;
; Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
; QY 7 CUGCCAGUCUCUT 20
; Db 1 CTGCCAGTCCT 14

; RESULT 10
; US-08-859-998-1273/C
; Sequence 1273, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; NUMBER OF SEQIDNOS: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:

; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; US-08-859-998-1273

; QUERY MATCH:
; Query Match 64.8%; Score 13.6; DB 2;
; Best Local Similarity 55.0%; Pred. No. 2.3e+03;
; Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
; QY 1 UAGGACUCGCCAGUCUCUT 20

; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101_1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO: 48278
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-48278

US-09-396-196G-52121

; QUERY MATCH:
; Query Match 66.7%; Score 14; DB 4; Length 25;
; Best Local Similarity 71.4%; Pred. No. 1.4e+03;
; Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
; QY 7 CUGCCAGUCUCUT 20
; Db 18 CTGCCAGTCCT 5

; RESULT 8
; US-09-396-196G-52121/c
; Sequence 52121, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101_1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 52121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-52121

; QUERY MATCH:
; Query Match 66.7%; Score 14; DB 4; Length 25;
; Best Local Similarity 71.4%; Pred. No. 1.4e+03;
; Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
; QY 7 CUGCCAGUCUCUT 20
; Db 1 CTGCCAGTCCT 14

; RESULT 10
; US-08-859-998-1273/c
; Sequence 1273, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; NUMBER OF SEQIDNOS: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:

; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; US-08-859-998-1273

; QUERY MATCH:
; Query Match 64.8%; Score 13.6; DB 2;
; Best Local Similarity 55.0%; Pred. No. 2.3e+03;
; Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
; QY 1 UAGGACUCGCCAGUCUCUT 20

Db 20 T⁹G⁶C²T¹G³C⁵G⁷G⁸T¹⁰T¹¹ 1

RESULT 11
US-08-859-998-1326
; Sequence 1326, Application US/08859998
; Patent No. 5934076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Brett E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 1273:
; US-09-225,928-1273
; Query Match 64.8%; Score 13.6; DB 2; Length 26;
; Best Local Similarity 55.0%; Pred. No. 2.3e+03;
; Matches 11; Conservative 5; Mismatches 4;
; Matches 13; Conservative 3; Mismatches 4;
; Indels 0; Gaps 0;
; Qy 2 AGGACCCUGCCACTAGCUCUTT 21
; Dy 4 AGGACCCCTCCAGCTACTT 23
; RESULT 12
; US-09-225,928-1326
; Sequence 1326, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37, 620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1326:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: DNA
FEATURE: OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1326:
US-09-225-928-1326
Query Match 64.8%; Score 13.6; DB 3; Length 26;
Best Local Similarity 65.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 AGGACCCGGCAGUCUTT 21
Db 4 AGGACCTTCAGCTACTT 23
RESULT 14
US-09-225-201B-1273/c
Sequence 1273, Application US/09225201B
Patent No. 6489455
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Disquette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37, 620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1326:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: DNA
FEATURE: OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1326:
US-09-225-201B-1273
Query Match 64.8%; Score 13.6; DB 4; Length 26;
Best Local Similarity 65.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UAGGACCCGGCAGUCUTT 20
Db 20 TTGGCTTGCCGGNGCTT 1
RESULT 15
US-09-225-201B-1226
Sequence 1326, Application US/09225201B
Patent No. 6489455
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Disquette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37, 620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1273:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: DNA
FEATURE: OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1326:
US-09-225-201B-1326
Query Match 64.8%; Score 13.6; DB 4; Length 26;
Best Local Similarity 65.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Fri Sep 30 14:33:41 2005

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Page 6

Search completed: September 30, 2005, 11:06:11
Job time : 124 secB


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RESULT 2
; Sequence 107545, Application US/10809189
US-10-809-189-107545
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101-1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40269
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-107545

Query Match
Best Local Similarity 75.2%; Score 15.8; DB 21; Length 25;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGGACUGCCAGUGUCUT 20
Db 1 AAGAGCTGCCAGTGCTT 19

RESULT 3
US-10-719-900-424586/c
; Sequence 424586, Application US/1071990
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 902914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 424586
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-424586

Query Match
Best Local Similarity 60.0%; Score 15.2; DB 21; Length 25;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 UAGGACCGCCAGUGUCUT 20
Db 21 TTGGACCTGCCAGTAATCTT 2

RESULT 4
US-10-809-189-40269
; Sequence 40269, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101-1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40269
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-40269

Query Match
Best Local Similarity 66.7%; Score 14.8; DB 21; Length 25;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TAGGAACCTGCCAGTGTTC 18
Db 2 TAGGAACCTGCCAGTGTTC 19

RESULT 5
US-10-809-189-55195
; Sequence 55195, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101-1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55195
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-55195

Query Match
Best Local Similarity 66.7%; Score 14.8; DB 21; Length 25;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GACCUCCAGUGUCUT 21
Db 7 GAGCTGCCCTGCTCTT 24

RESULT 6
US-10-809-189-55196
; Sequence 55196, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

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; FILE REFERENCE: 3101_1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIORITY APPLICATION NUMBER: US/09/336,196
; PRIORITY FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 55196
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-10-809-189-55196
; Query Match 70.5%; Score 14.8; DB 21; Length 25;
; Best Local Similarity 66.7%; Pred. No. 1.5e+03; 4; Mismatches 2; Indels 0; Gaps 0;
; Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
; Qy 4 GACCUGGCCAGGUCCU 21
; Db 1 GACCTGCCGTCCTT 18
; ;
; RESULT 7
; US-10-956-157-154607
; Sequence 154607, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: weth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 01896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 154607
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-154607
; Query Match 70.5%; Score 14.8; DB 21; Length 25;
; Best Local Similarity 66.7%; Pred. No. 1.5e+03; 4; Mismatches 2; Indels 0; Gaps 0;
; Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
; Qy 2 AGGACCUCCAGGUCCU 19
; Db 4 AGGATCTGAGCTCT 21
; ;
; RESULT 8
; US-10-719-956-56046
; Sequence 56046, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; TITLE OF INVENTION: Methods of Determining a Signature of a
; FILE REFERENCE: 53525-8040.US00
; CURRENT APPLICATION NUMBER: US/10/407,089
; CURRENT FILING DATE: 2003-04-02
; PRIORITY APPLICATION NUMBER: US/09/654,187
; PRIORITY FILING DATE: 2000-09-01
; PRIORITY APPLICATION NUMBER: US 60/182,454
; PRIORITY FILING DATE: 2000-02-15
; PRIORITY APPLICATION NUMBER: PCT/US98/11224
; PRIORITY FILING DATE: 1998-05-22
; PRIORITY APPLICATION NUMBER: US 08/862,610
; PRIORITY FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: encoded adaptor
; FEATURE: OTHER INFORMATION: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1)..(28)
; OTHER INFORMATION: n = A,T,C or G
; US-10-719-956-56046
; Query Match 69.5%; Score 14.6; DB 17; Length 28;

i ORGANISM: mus musculus
US-10-809-189-48277

Query Match 68.6%; Score 14.4; DB 21; Length 25;
Best Local Similarity 68.8%; Pred. No. 2.4e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 5 ACCUGGCCAGUGCUCU 20
|:||||||:||:||:
Db 2 AACCTGCCAGTGCTT 17

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Title:

US-10-738-413-1

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3: gb_htc:
4: gb_est3:
5: gb_est4:
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8: gb_gb1:
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871: gb_gb864:
872: gb_gb865:
873: gb_gb866:
874: gb_gb867:
875: gb_gb868:
876: gb_gb869:
877: gb_gb870:
878: gb_gb871:
879: gb_gb872:
880: gb_gb873:
881: gb_gb874:
882: gb_gb875:
883: gb_gb876:
884: gb_gb877:
885: gb_gb878:
886: gb_gb879:
887: gb_gb880:
888: gb_gb881:
889: gb_gb882:
890: gb_gb883:
891: gb_gb884:
892: gb_gb885:
893: gb_gb886:
894: gb_gb887:
89

RESULT 2	
LOCUS	AZ821702
DEFINITION	2M009401R Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC2M0094001 R, genomic survey sequence.
ACCESSION	AZ821702
VERSION	AZ821702.1 GI:12991610
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
COMMENT	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meinen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederauer,A. and Wright,D.; weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
CONTACT	Contact: Robert B. Weiss
UNIVERSITY	University of Utah Genome Center
ADDRESS	University of Utah 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
TELEPHONE	Tel: 801 585 5606
FAX	Fax: 801 585 7177
EMAIL	Email: cdunmogenetics.utah.edu
INSERT LENGTH	Insert Length: 10000 Std Error: 0.00
PLATE	Plate: 0094 row: O column: 01
SEQ PRIMER	Seq primer: CACACAGGAACAGCTATGACC
CLASS	plasmid ends
FEATURES	High quality sequence stop: 28.
SOURCE	Location/Qualifiers
1.	28
/organism="Mus musculus"	
/mol_type="genomic DNA"	
/db_xref="NC_057BLJ6J"	
/clone="UGGC2M0094001"	
/sex="Male"	
/lab_host="E. coli strain XL10-Gold, T ₁ -resistant, F-	
/clone_lab="Mouse 10kb Plasmid UGGC1M library"	
/note="Vector: PWD42Inv; Purified genomic DNA from M. musculus C57BL/6J (male)"	
Laboratory Mouse DNA Resource	
(http://www.jax.org/gj/documents/dnare/)	
The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA Polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 73214 gb AFL2072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
ORIGIN	
Query Match	58.1%; Score 12.2; DB 8; Length 28;
Best Local Similarity	58.8%; Pred. No. 3.8e+05;
Matches	10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY	3
DB	12
Db	GTACATGCCATTGCTCT 28
RESULT 3	
LOCUS	AG192441
DEFINITION	Pan troglodytes DNA, clone: RP43-068P22.T7, genomic survey sequence.
ACCESSION	AG192441
VERSION	AG192441.1 GI:45224617
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes
COMMENT	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Choi,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H. BAC end sequences of Library RP-43 Unpublished
AUTHORS	Part,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Choi,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE	Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daegjeon 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL: http://phs.grc.kribb.re.kr/ , Tel:82-42-666-7181, Fax:82-42-660-4409)
JOURNAL	Copies are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS	
LIBRARY	Sequencing: T7
FEATURES	
SOURCE	Vector : DBACE3_6
R.Site 1	: EcoRI
R.Site 2	: EcoRI
LOCATION/QUALIFIERS	
1.	-28
/organism="Pan troglodytes"	
/mol_type="genomic DNA"	
/db_xref="taxon:9598"	
/clone="RP43-068P22.T7"	
/sex="male"	
/cell_type="lymphocytes"	
/clone_lab="RP-43 Chimpanzee Male BAC Library"	
ORIGIN	
Query Match	58.1%; Score 12.2; DB 9; Length 28;
Best Local Similarity	58.8%; Pred. No. 3.8e+05;
Matches	10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY	3
DB	12
Db	GTACATGCCATTGCTCT 28
RESULT 4	
LOCUS	A137076
DEFINITION	A137076 Soares_pregnant uterus_NBHU Homo sapiens cDNA clone IMAGE:20417463, Similar to SW:1T4G_HUMAN Q04637_EUKARYOTIC TRANSLATOR INITIATION FACTOR 4 GAMMA ; mRNA sequence.
ACCESSION	A137076
VERSION	A137076.1 GI:4149529
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Mammalia; Eutheria; Primates; Cracini; Hominoidea; Homo
QY	4
DB	1
Db	GACCTGCCATACTATT 17

REFERENCE 1 (bases 1 to 28)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contract: Robert Strauberg, Ph.D.
 Email: cgabp@mail.nih.gov
 This clone is available royalty-free through LInL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 1306 Std Error: 0.00
 Seq primer: -dGDP from Gibco

FEATURES source
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .28

/organism="Homo sapiens"
/mol type="mRNA"
/db xref="Taxon:9606"
/clone="IMAGE:2041746"
/sex="Female"

/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NBHPU"
/clone:Lib="Soares_pregnant_uterus_NBHPU"
/notes="Orcan: uterus; Vector: pRT7T-Pac; Site 1: Not I -
site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligodT) primer [5, AACTGAGAATTCGGCCCTTTCCTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia, digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 55.2%; Score 11.6; DB 1; Length 28;
Best Local Similarity 61.1%; Pred. No. 7.4e+05;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCUCCAGUCU 19
Db 20 AGGACCACTACGGGCCTC 3

RESULT 5 AJ59231 LOCUS AJ59231 LINEAR DNA GSS 15-JAN-2004

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 69G01, genomic survey sequence.

ACCESSION AJ59231 VERSION AJ59231.1 GID:37941855

KEYWORDS GSS

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL University of Utah Genome Center

COMMENT Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 048 Row: B Column: 23

Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES source
1. .29

/organism="Mus musculus"
/mol type="genomic DNA"
/strain="57BL/6J"
/db xref="Taxon:10090"
/clone="UGC2M0148B23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG library"

to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES source
1. .22

/organism="Arabidopsis thaliana"
/cultivar="Wassilevskija"
/db xref="Taxon:3702"
/clone="69G01"
/clone_id="Arabidopsis thaliana T-DNA insertion lines"
/notes="T-DNA flanking sequence
right border"

ORIGIN

Query Match 52.4%; Score 11; DB 9; Length 22;
Best Local Similarity 57.9%; Pred. No. 1.4e+06;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGACCUCCAGUCU 21
Db 3 GGACTGCCAGCTCTT 21

RESULT 6 AJ2847949 LOCUS AJ2847949 LINEAR DNA GSS 21-FEB-2001

DEFINITION 2M0148B2R Mouse 10kb plasmid UGCG library Mus musculus genomic clone UGCG2M0148B23 R, genomic survey sequence.

ACCESSION AJ2847949

VERSION AJ2847949.1 GID:13029307

KEYWORDS GSS

SOURCE

ORGANISM Mus musculus (house mouse)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL University of Utah Genome Center

COMMENT Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 048 Row: B Column: 23

Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES source
1. .29

/organism="Mus musculus"
/mol type="genomic DNA"
/strain="57BL/6J"
/db xref="Taxon:10090"
/clone="UGC2M0148B23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG library"

REFERENCE 1 (bases 1 to 22)
 AUTHORS Direct Submission
 TITLE JOURNAL Submitted (23-OCT-2003) Balzergue S., INRGV, INRA/CNRS, 2 rue Gaston Crémieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Verbaillies). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border

/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnare/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.4%; Score 11; DB 8; Length 29;
Best Local Similarity 57.9%; Pred. No. 1.4e+06;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AGGACCUCCAGGUCUT 20
Db 8 ATGACCTGCCATGATCAT 26

RESULT 7

LOCUS AZ815857 26 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0084A01F Mouse 10kb plasmid UGGCIM library Mus musculus genomic
CLONE UGGC2M0084A01 F, genomic survey sequence.
ACCESSION AZ815857
VERSION AZ815857.1 GI:12985765
KEYWORDS GSS,
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCES 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
COMMENT Contact: Robert B. Weiss
JOURNAL University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0084 Row: A Column: 01
Seq primer: CCTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source
1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="Taxon:10090"
/clone="UGGC2M0084A01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCIM library"

ORIGIN

Query Match 51.4%; Score 10.8; DB 8; Length 26;
Best Local Similarity 64.3%; Pred. No. 1.8e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 8 UGCCAGGUCUTT 21
Db 19 TGCCAGGGTTT 6

RESULT 8

LOCUS AZ617463 24 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0448F15R Mouse 10kb plasmid UGGCIM library Mus musculus genomic
CLONE UGGC1M0448F15 R, genomic survey sequence.
ACCESSION AZ617463
VERSION AZ617463.1 GI:11739653
KEYWORDS GSS,
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCES 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
COMMENT Contact: Robert B. Weiss
JOURNAL University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0448 Row: F Column: 15
Seq primer: CACACGAGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source
1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="Taxon:10090"
/clone="UGGC1M0448F15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCIM library"

/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnare/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C5BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|47321149b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match Score 50.5%; Score 10.6; DB 8; Length 24;
Best Local Similarity 70.6%; Pred. No. 2.2e+06;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCUCCAGUCUC 18
Db |||| :||||||| 2
18 AGGAATGCCAACGCAC 2

RESULT 9

AL042578 AL042578 28 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZP434J0821_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION AL042578
VERSION AL042578.1
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 28)
AUTHORS Blum,H., Bauerachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

FEATURES location/Qualifiers
source
1. .28
/organism="Homo sapiens"
/mol_type="genomic DNA"
/strain="C5BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM050N01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C5BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|47321149b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match Score 49.5%; Score 10.4; DB 1; Length 28;
Best Local Similarity 61.5%; Pred. No. 2.8e+06;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCUGCCAGUCUC 18
Db |||| :||||||| 15
3 CCTGCCNGTACTC 15

Locus AZ642513 28 bp DNA linear GSS 14-DBC-2000
Definition IM050N01R Mouse 10kb plasmid UGGCM library Mus musculus genomic
Definition clone UGGCM050N01 R, genomic survey sequence.
Accession AZ642513
Version AZ642513.1 GI:1176194
Keywords GSS.

Source Mus musculus (house mouse)
Organism Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Reference 1 (bases 1 to 28)
Authors Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud.M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Title Mouse whole genome scaffolding with paired end reads from 10kb plasmid insert
Journal Unpublished (2000)
Comment Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0505 column: 01
Seq primer: CACCAAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
Source
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C5BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM050N01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C5BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|47321149b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match Score 49.5%; Score 10.4; DB 8; Length 28;
Best Local Similarity 75.0%; Pred. No. 2.8e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCGAGGUCCUT 20
Db |||| :||||||| 14
3 GCCAGAGCTCT 14

Result 11
A2642513

LOCUS	AZ54477	29 bp	DNA	linear	GSS 04-OCT-2000	LOCUS	BG24013	30 bp	mRNA	linear	EST 14-MAR-2001
DEFINITION	IM0256N22F Mouse 10kb plasmid UNGC1M library Mus musculus genomic	602447475F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4586106 5'	DEFINITION	602447475F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4586106 5'	DEFINITION	mRNA sequence.	mRNA sequence.				
ACCESSION	AZ54477					ACCESSION	BG24013				
VERSION	AZ54477.1					VERSION	BG24013.1				
KEYWORDS	GSS.					KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)					SOURCE	Homo sapiens (human)				
ORGANISM	Mus musculus					ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 29)					REFERENCE	1 (bases 1 to 30)				
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenin, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.					AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts					TITLE	Unpublished (1999)				
JOURNAL	Unpublished (2000)					JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Contact: Robert B. Weiss					COMMENT	Contact: Robert Straussberg, Ph.D.				
University of Utah Genome Center						Tissue Procurement: DCMP/DTP	Email: cgapbs-r@mail.nih.gov				
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT						cDNA Library Preparation: Ling Hong/Rubin Laboratory					
Tel: 801 585 5606						cDNA Sequencing by: The T.M.A.G.E. Consortium (LLNL)					
Fax: 801 585 7177						Clone distribution: MGC clone distribution information can be					
Email: ddunng@genetics.utah.edu						found through the T.M.A.G.E. Consortium/LLNL at:					
Insert length: 10000 Std Error: 0.00						http://image.llnl.gov					
Plate: 0256 row: N column: 22						Plate: LLNL314 row: e column: 19					
Seq primer: CCTTGTAACAGCGGCCAGT						High quality sequence stop: 29.					
Class: Plasmid ends						High quality sequence stop: 30.					
FEATURES	Location/Qualifiers					FEATURES	Location/Qualifiers				
SOURCE	1..29					SOURCE	1..30				
/organism="Mus musculus"						/organism="Homo sapiens"					
/mol_type="genomic DNA"						/mol_type="mRNA"					
/strain="CS7BL/6J"						/db_xref="taxon:9606"					
/db_xref="taxon:10090"						/lab_host="DH10B (phage-resistant)"					
/clone="UNGCI1M0256N22"						/clone="IMAGE:4586106"					
/sex="Male"						/clone="HOMO:DH10B (phage-resistant)"					
/lab_host="E. Coli strain XL10-Gold, Tr-resistant, F+						/clone_lib="NIH_MGC_14"					
/clone_id="Mouse 10kb plasmid UNGC1M library"						/note="Organ: kidney; Vector: pMB7; Site 1: XbaI; Site 2:					
/note="Vector: PWD421V; Purified genomic DNA from M.						ECOR1; cDNA made by oligo dT priming. Directionally					
musculus C57BL/6J (male)" was obtained from the Jackson						cloned into EcoRI/XbaI sites using the following 5'					
Laboratory Mouse Resource						insert size 1.8kb. Library constructed by Ling Hong in					
(http://www.jax.org/resources/documents/dnares/).						the laboratory of Gerald M. Rubin (University of					
The DNA was hydrodynamically sheared by repeated passage through a						California, Berkeley) using ZAP-cDNA synthesis kit					
0.005 inch orifice at constant velocity. The sheared DNA						(Stratagene) and Superscript II RT (Life Technologies)."					
was blunt end repaired with T4 DNA polymerase and T4											
polynucleotide kinase. Adaptor oligonucleotides were											
ligated to the blunt ends in high molar excess. The											
adapted DNA was purified and size selected for a 9.5 to											
10.5 kb range using preparative agarose gel											
electrophoresis. Vector DNA was prepared from a derivative											
of pWD42 (gi 473214 gb AF120972.1), a copy-number											
inducible derivative of plasmid RL. The vector was ligated											
with adaptors complementary to the insert adaptors and											
puri fied. The sheared, adapted mouse DNA was annealed to											
adapted vector DNA, and transformed into											
chemically-competent E. coli XL10-Gold (Stratagene) cells											
and selected for ampicillin resistance."											
ORIGIN	RESULT 13					ORIGIN	RESULT 13				
Query Match	49.5%	Score 10.4;	DB 8;	Length 29;		Query Match	49.5%	Score 10.4;	DB 4;	Length 30;	
Best Local Similarity	75.0%	Pred. No.	2.8e+06;			Best Local Similarity	55.0%	Pred. No.	2.8e+06;		
Matches	9;	Conservative	2;	Mismatches 1;	Indels 0;	Mismatches	11;	Conservative	3;	Mismatches 6;	Indels 0;
Qy	7	CATGCCAGAUGUC 18				Qy	2	AGGACCCGCAAGUC 21			
Db	29	CGGCCAGTC 18				Db	30	AGTAACGCAATGCTTT 11			
RESULT 12	AZ2603158/c					RESULT	AZ2603158				
ORGANISM	Mus musculus					ORGANISM	Mus musculus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 22)					REFERENCE	1 (bases 1 to 30)				
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenin, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.					AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts					TITLE	Unpublished (1999)				
JOURNAL	Unpublished (2000)					JOURNAL	Contact: Robert Straussberg, Ph.D.				
RESULT 12	BG424013/c					RESULT	BG424013				

COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dduan@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0422 row: L column: 13 Seq primer: CGTGTAAACGACGCCAGT Class: plasmid ends
FEATURES	High quality sequence stop: 22. Location/Qualifiers
SOURCE	1. .22 /organism="Mus musculus" 'mol_type="genomic DNA" 'strain="C57BL/6J" 'db_xref="taxon:10090" 'clone="UUCM042L13" 'lab_host="E. coli strain XU10-Gold, T1-resistant, F-" 'clone_lib="Mouse 10kb plasmid UUCM library" 'note="vector: pMD42mv; Purified genomic DNA from M. musculus C57BL/6J (male)" 'sex="Male" 'lab_host="E. coli strain XU10-Gold, T1-resistant, F-" 'clone_lib="Soares_NFL_T_GBC_S1" 'note="Organ: pooled; Vector: pMT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH119W, testis NHT, and B-cell NCI CGAP Gb1) were mixed, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 294480-302087, 682632-687239, 726408-728711, and 729096-73199. Subtraction by Bentol Soares and M. Fatima Bonaldo."
ORIGIN	Query Match Score 48.6%; Score 10.2; DB 8; Length 22; Best Local Similarity 53.3%; Pred. No. 3.4e+06; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0; QY 6 CCUGCCAGUCUC 20 Db 18 CCTTCCTCTCT 4
RESULT 14	Query Match Score 48.6%; Score 10.2; DB 8; Length 22; Best Local Similarity 53.3%; Pred. No. 3.4e+06; Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
DEFINITION	YAC clone YMWIR121D10, genomic survey sequence.
ACCESSION	AB004341
VERSION	AB004341.1 GI:2242909
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (site:6) Yoshino,M., Xiao,H., Jones,E., Trachtulec,Z., Vincek,V., Flaherty,L. and Fischer Lindahl,K.
AUTHORS	
TITLE	A YAC contig from the distal Mhc class I region on mouse Chr17 Unpublished
JOURNAL	
REMARKS	2 (bases 1 to 28)
AUTHORS	Yoshino,M.
TITLE	Direct Submission
JOURNAL	Submitted (29-MAY-1997) Masayasu Yoshino, U.T. Southwestern Medical Center, HMM, 5323 Harry Hines Blvd, Dallas, TX 75235-9050, USA (E-mail: YOSHINO@UTSW.SWMBD.EDU, Tel:214-648-5047, Fax:214-648-5533)
FEATURES	Location/Qualifiers
SOURCE	1. .28 /organism="Mus musculus" 'mol_type="genomic DNA" 'strain="C57BL/6J" 'db_xref="taxon:10090" 'chromosome="17" 'clone="YAC YMWIR121D10" 'haplotypes="H2b" 'clone_lib="the MIT mouse YAC library; cat. #95021 Research Genetics" 'note="right arm portion of the clone"
ORIGIN	Email: cgabbs-remail.nih.gov

Query Match 48.6%; Score 10.2; DB 9; Length 28;
Best Local Similarity 53.3%; Pred. No. 3.5e+06;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 5 ACCUGCCAGUGCUU 19
Db 10 ACCTGGCACTTCCTT 24

Search completed: September 30, 2005, 11:04:02
Job time : 2992 secs